AMENDMENTS TO THE CLAIMS:

The following listing of claims replaces all prior listings, and all prior versions, of claims in the application.

LISTING OF CLAIMS:

1. -7. (Cancelled).

8. (Currently amended) A method for gene expression analysis ~~of genes derived from different samples,~~ comprising:

preparing first nucleotides including a targeted gene by using a first sample and introducing a first base sequence and a second base sequence, which are nonspecific to the base sequence of the targeted gene, to the targeted gene so that the second base sequence is bound to a position closer to the 5' end than is the first base sequence, said first sample being derived from a first specimen,

preparing second nucleotides including the targeted gene by using a second sample and introducing a third base sequence and the second base sequence, which are nonspecific to the base sequence of the targeted gene, to the targeted gene so that the second base sequence is bound to a position closer to the 5' end than is the third base sequence, said second sample being derived from a second specimen~~different from the first sample~~,

mixing the first nucleotides and the second nucleotides,

subjecting the first nucleotides and the second nucleotides to nucleic acid amplification using a primer comprising a base sequence specifically hybridizing to the targeted gene, a primer comprising a base sequence identical to the second base sequence, a first probe comprising a base sequence identical or complementary to the first base sequence, and labeled at one end with a first

fluorophore and at another end with a quencher, a second probe comprising a base sequence identical or complementary to the third base sequence, and labeled at one end with a second fluorophore and at another end with a quencher, and thermostable DNA polymerase having 5'→3' exonuclease activity,

digesting the first probe and the second probe bound to the first base sequence and the third base sequence, by the thermostable DNA polymerase at the time of the nucleic acid amplification, and

detecting a fluorescence emitted by the first fluorophore and the second fluorophore released in digesting the first probe and the second probe, thereby assaying the amount of the product of the nucleic acid amplification,

wherein a sequence of the targeted gene included in the first nucleotides and a sequence of the targeted gene included in the second nucleotides are the same.

9. (Previously presented) The method for gene expression analysis according to claim 8, wherein the first nucleotides are synthesized by introducing the first base sequence and the second base sequence into the targeted gene using a primer, which comprises the first base sequence, which is closer to the 5' end than a fourth base sequence comprising a sequence that specifically hybridizes to the targeted gene, and the second base sequence, which is closer to the 5' end than the first base sequence, and wherein the second nucleotides are synthesized by introducing the third base sequence and the second base sequence into the targeted gene using a primer, which comprises the third base sequence, which is closer to the 5' end than the fourth base sequence comprising a sequence that specifically hybridizes to the targeted gene, and the second base sequence, which is closer to the 5' end than the first base sequence.

10. (Previously presented) The method for gene expression analysis according to claim 8, wherein the first nucleotides are cDNA comprising the first base sequence and the second base sequence introduced therein by subjecting mRNA of the targeted gene to reverse transcription using a primer which comprises the first base sequence, which is closer to the 5' end than a fourth base sequence comprising a sequence that specifically hybridizes to the targeted gene and the second base sequence, which is closer to the 5' end than the first base sequence, and wherein the second nucleotides are cDNA comprising the third base sequence and the second base sequence introduced therein by subjecting mRNA of the targeted gene to reverse transcription using a primer which comprises the third base sequence, which is closer to the 5' end than the fourth base sequence comprising a sequence that specifically hybridizes to the targeted gene and the second base sequence, which is closer to the 5' end than the third base sequence.

11. (Previously presented) The method for gene expression analysis according to claim 8, wherein the Tm values of the first probe and the second probe are substantially the same.

12. (Cancelled).

13. (New) The method for gene expression analysis according to claim 8, wherein said second specimen is a different specimen than said first specimen.

14. (New) A method for gene expression analysis comprising:

preparing first nucleotides including a targeted gene by using a first sample and introducing a first base sequence and a second base sequence, which are nonspecific to the base sequence of the targeted gene, to the targeted gene so that the second base sequence is bound to a position closer to the 5' end than is the first base sequence, said first sample being derived from a first tissue or organ,

preparing second nucleotides including the targeted gene by using a second sample being different from the first sample and introducing a third base sequence and the second base sequence, which are nonspecific to the base sequence of the targeted gene, to the targeted gene so that the second base sequence is bound to a position closer to the 5' end than is the third base sequence, said second sample being derived from a second tissue or organ,

mixing the first nucleotides and the second nucleotides,

subjecting the first nucleotides and the second nucleotides to nucleic acid amplification using a primer comprising a base sequence specifically hybridizing to the targeted gene, a primer comprising a base sequence identical to the second base sequence, a first probe comprising a base sequence identical or complementary to the first base sequence, and labeled at one end with a first fluorophore and at another end with a quencher, a second probe comprising a base sequence identical or complementary to the third base sequence, and labeled at one end with a second fluorophore and at another end with a quencher, and thermostable DNA polymerase having 5'→3' exonuclease activity,

digesting the first probe and the second probe bound to the first base sequence and the third base sequence, respectively, by the thermostable DNA polymerase at the time of the nucleic acid amplification, and

detecting a fluorescence emitted by the first fluorophore and the second fluorophore released in digesting the first probe and the second probe thereby assaying the amount of the product of the nucleic acid amplification,

wherein a sequence of the targeted gene included in the first nucleotides and a sequence of the targeted gene included in the second nucleotides are the same.

15. (New) The method for gene expression analysis according to claim 14, wherein said second tissue or organ is a different tissue or organ than said first tissue or organ.